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GenCore version 5.1.3
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OM protein - pretein search, using sw model

January 16, 2003 16-40-32 - Search time 43 7143 Seconds Run on.

(without alignments) 56.562 Million rell apdates/ser

US-09-856-070-21 60 Perfect score:

1 EFLMLRLODYEE 12 Sequence:

RLOSUM62 Gapop 10 0 , Gapext 0 5 Scoring table:

671580 segs, 206047115 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Mayirum DB seq length: 20000000mm

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp_archea:* SPTREMBL_21:* Database :

sp_unclassified.* sp_invertebrate:* sp_vertebrate:* sp_rvirus:* sp_bacteriap:* sp_bacteria:*
sp_tungi:*
sp_human:* sp_organelle:* sp rovient⋅* sp_virus:* sp_phage:* sp_plant:* sp_mammal:* sp_mhc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the refal score distribution

sp_archeap:*

SUMMARIES

Description	deides omod Stogbo	Oguizé homo sapien	Ulusam sam 1,500	Oguiz7 homo sapien	OBYBK3 rattus norv	TIES STITES AMBANO	OBOXXE FOR FOLDER	Oghru0 halobacteri	095qw7 caenorhabdi	P78514 homo sapien	099854 homo sapien	055449 synechooyst	09xis3 bacteriopha	DAYKAG BOMO Sapien	29.25.43.145.145.15	Q9k660 bacillus ha
01	оветя	090.126	09DC11	090327	QRVHK3	O SYCWA	PAXAPO	Q9HRU0	0950W7	P78514	099854	055449	Q9XJS3	nakada	CA JUNE	Q9K660
H _C	4	4	Ξ	₹	Ξ.		~	17	5	4	4	C	ō	4	ş	16
Query Match Lendth DB	ጉጸብ	159	586	158	4.55	ιc· α ιc·	4.5	250	376	429	453	5.84	634	, ,	à	130
Query Match	100 0	95.0	95.0	91.7	88.3	75.0	66.7	65.0	65.0	65.0	65.0	0.59	65.0	55.0	6.8.7	63.3
Score	09	57	57	55	53	45	40	39	39	39	39	30	39	3.0	38	38
Result No.	7	C1	~	ব	S	9	7	œ	9	10	1.1	12	13	14	15	16

159 AA.

P.R.T.;

PRELIMINARY;

Ç38456 10 Q98386

RESULT 2

Q8uhe2 agrobacteri	095kl8 madada faso	Q8wp20 macaca tasc	Q96m50 homo sapien	Q91480 salmo salar	Q8t5i7 anopheles q	020766 paenorhabdi	064106 bacteriopha	034838 bacillus su	CASES Lingin Luha	Q9u]z8 homo sapien	Q99K28 Esmo sapien	Seniu2 pyrococnus		۲.	- 17	Q52534 pseudomonas	O9pgs2 xylella fas	066941 aquifex aco	O8t3h6 drosophila	Q9vpl8 drosophila	Q91748 xenopus lae	Q8qnh5 ectocarpus	CORXES STILLLOWYCE	0974u8 sulfolobús	Q8svc8 encephalito	Q9h:42 pseudomonas	Q9zuul arabidopsis	P78849 schizosacch
Q8UHE2	Q95K1R	ORMECO	Q96M50	3 Q91480	087517	020766	064106	5 034838	045212	Q9UJZ8	OBLIKSO				081900	052534	0.09PCS2	066941	Q8T3H6	O9VFL8	3 091748			7 097408	SRXV13		0 092001	P78849
50 16	311 6	476 C	56 4	.058 13	1200 5	363 5	5	111 16	F 1	56 4	16: 4		231 17	81 17	es G	0.6		37 16	18 5	443 5		65 12	187 16	249 17	4 h	91 097	84 10	327 3
	~			10	F 4	3 13				,		C1	7		C4 _	.~				4	4							
63.3	63.3	5.5	63.3	63.3	3	63.3	61.7		Ω .7	61.7	61.3	61.7	61.7	61.7	61.7	61.7	61.7	61.7	61.7	61.7	61.7	61.7	() () ()	0.09	0.9	60.0	0.09	0.09
38	38	ν, Ω	38	3.8	3.8	æ 7	2.7	3.7	7.7	3.7	3.7	3.7	3.7	3.7	3.7	7.	3.7	3.7	37	3.7	3.7	3.7	₹: *:	36	ن بر	36	3.6	36
17	18	⊕ -1	20	21	C1	23	· ·	25	55	2.7	90	ž.	30	31	3.5	æ æi	3.4	35	36	4.7	38	39		4.1	4.2	~ ₹1"	44	4 5

ALIGNMENTS

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                                                                                                                             Homo sapiens (Human).
Eukaryota; Metarca; Chordata; Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primales; Calarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                         Strausberger R.;

Submitted (SEP 2001) to the EMRI/GenRank/DDBJ databases.

R EMBJ; BC013903; AAM13903.1; -..

R InterPro: IPR000299; Band_4.1; -..

R InterPro: IPR000799; Band_4.1; -..

R Pfam; PF00779; Hand_41; 1...

P Pfam; PF00779; Hand_41; 1...

P PROSITE: PS00569; EMND_41_1; UNKNOWN_1.

PROSITE: PS00561; BAND_41_2; UNKNOWN_1.

PROSITE: PS00561; BAND_41_2; UNKNOWN_1.

PROSITE: PS00561; BAND_41_3; 1...

PROSITE: PS00561; BAND_41_3; 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%: Score 60, DB 4; Length 586;
Line 10x; Pred No. 9.912;
Line 0, Mishatches 6; Indels
                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                 PRT;
                                                                                                                 Similar to villin 2 (ezrin).
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                                 PRELIMINARY;
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345 EELMLRLQDYEE 356
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es 12, Comserv
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                  NCBI_TaxID-9606;
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                              996008
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RESULT 1
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Andrawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Andrawa T., Hara A., Fukuhishi Y., Konno H., Adachi J., Fukuda S.,
Anirawa K., Izawa M., Nishi K., Kiyoswa H., Nondo S., Yamanaka I.,
Anirawa K., Matsuda H.A., Ashburner M., Bahalov S., Casavant T.,
Kadola K., Matsuda H.A., Ashburner M., Bahalov S., Casavant T.,
Redola K., Matsuda H.A., Ashburner M., Bahalov S., Casavant T.,
Redola K., Matsuda H.A., Ashburner M., Bahalov S., Casavant T.,
Ruchi P., Icwis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Sakani K., Okido T., Furuno M., Aono H., Haddarelli R., Harsh G.,
Sakai K., Okido T., Furuno M., Aono H., Haddarelli R., Marsh G.,
Sakai K., Okido T., Furuno M., Aono H., Haddarelli R., Marsh G.,
Sakai K., Okido I., Bolunda N., Carninci P., de Booaldo M. F.,
Gustincich S., Hill D., Hohmann M., Hume D.A., Kamiya M., Lee N.H.,
Gustincich S., Hill D., Hohmann M., Mazzarcili J., Mombaerts P.,
Nordone P., Ring H., Mingwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schochaek U., Shibata Y., Shibata Y., Shiorch K. F.,
Nyashay-Boolis A., Yoshida K., Haseqawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sdety
                                                                                                                                      Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; VerLebrata; Euteleostomi;
Mammalla; Eutheria; Kodentia; Sciurognathi; Muridao; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 2), Last annotation update)
Adult male kidney CDNA, RIKEN full-length enriched library,
clone:0610037422, fill insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 95.0%; Score 57: DB 4: Length 159;
Best Local Similarity 91.7%; Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0. Inde]s
                                                                                                                                                                                                                                                                                                                                    "Mutation of ezrin gene in cancer.";
Submitted (SEP-1999) to the EMBL/GenHank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              159 AA; 19234 MW; 7C398388H7HA70FA CRC64;
                    01-MAY-2000 (TrEMBLrel. 1%, Created)
01-MAY-2000 (TrEMBLrel. 1%, Last sequence update)
01-MAK-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       586 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel, 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000798; EZ/rad/moesin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P.R.1 ;
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Fadiel A., Chen Z.C., Naltolin F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-C57BL/61; TISSUE-KIDNEY;
MEDLINE-21085660; Pubmed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plam; PF00769; ERM; 1.
PROSITE; PS50057; BAND_41_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 409:685-690(2001).
EMBL: AKO02765; HAB22341:1; -.
                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF189213; AAF03156.1; -...
InterPro; IPR000299; Band_4.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:98931; Vil2.
InterPro; IPR000299; Band_4.1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    159
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                                                                                                              Ezrin (Fragment).
                                                                                                                                                                                                                            NCB1_Tax1D-9606;
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sápieńs (Húman).
Fukaryota; Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eskaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                0
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:
                                                                                                                                                                                                                  95.0%; Score 57; DH 11; Length 586; 91.7%; Pred, No. 0.041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.7%; Score 55; DB 4; Longth 158; 100.0%; Pred. No. 0.025; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen Z.C., Fadiel A., Naftolin F.; "Exin dene mutalion in ovarian cancer."; Submitted (EPP-1999) for the EMBL/GenBank/DDBJ databases. EMBL AF1888897; AAF03155.1; "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-SPRAGUE-DAWLEY;
GUND MOORE F.J., Tait S., Brophy P.J.;
Submitted (NOV-2001) to the EMBL/GenBank/PDBJ databases.
                                                                                                      PROSITE; PS00660; BAND_41_1; 1.
PROSITE; PS00661; BAND_41_2; 1.
PROSITE; PS50057; BAND_41_3; 1.
SEQUENCE: 586 AA: 69434 MW; 591AH8F575F6DE3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19086 MW; 8689281806829578 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2002 (TrEMBLrel. 20, Last asnotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAR-2002 (TrEMBLEd), 20, Greated)
01-WAR-2002 (TrEMBLEd), 20, Last sequence update)
01-JUN-2002 (TrEMBLEd), 21, Last annotation update)
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                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.
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InterPro, 1PR060798; Ez/rad/moesin.
Pfam; PF00769; ERM; 1.
InterPro; IPK000798; E2/rad/moesin.
Ptam; PF00373; Band_41; 1.
Pfam; PF00769; ERM: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF450298; AAL47844.1; -.
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Best Local Similarity 91.77
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Conservative
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                                                                 PRINTS; PR00935; BAND41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norveqicus (Rat).
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345 ERLMLRLQDYEQ 356
                                                                                                                                                                                                                                                                                                      1 EELMLRLODYER 12
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                                                                                        841;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ezrin (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-9606;
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                                                                                        SMART; SM00295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11SSUE-OVARY;
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NON_IER
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Gaps

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A MEDLINE_PEON N.A.

MEDLINE_20504483; Pubmed 11015950;

RA MEDLINE_20504483; Pubmed 11015950;

RA Shakla H D., Lasky S.R., Baliga N S., Thorsson V., Sbrogna J.,

RA Shakla H D., Lasky S.R., Baliga N S., Thorsson V., Sbrogna J.,

RA Letbauser B., Keller K., Cruz R., Danson M.J., Bough D.W.,

RA Maddocks D.G., Tablonski P E., Krebs M.P., Angevine C M., Dale B.,

RA Alam M., Freitas T.A., Peck R.E., Pohlschroder M., Spudich J.L., Jung K.-B.,

RA Alam M., Freitas T. How T.M., idang P., Rijey M., Hood L., Dassarma S.,

RA Ebhardt H., Lowe T.M., idang P., Rijey M., Hood L., Dassarma S.,

RT "Genome sequence of Halobacterium species NRC-1.";

"The Math. Acad. Sci. C.S.A., 97.12176 12181(2000).
Actinopterggii, Neopterggii, feleostei, Euteleostei, Neoteleostei;
Acanthomotpha, Acanthopterggii, Percomorpha; Tetraodontiformes;
Tetraodontidae; Takituqu.
                                                                                                                                                                                                                                                                                         "Conserved syntemy between the Fugu and human PTEN locus and the evolutionary equisoration of vertebrate FTEN function.";
                                                                                                                                                                                            MEDIJNE-21455582; PubMed-11571655;
Yu W.P., Pallen C.J., Tay A., Jirik F.R., Brenner S., Ian Y.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.0%, Store 39, DB 17; Length 250; 66.7%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.7%; Score 40; DB 13; Length 534; 58.3%; Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Halobacterium sp. (strain NRC-1).
Archaea; Euryarchacota; Halobacteria; Halobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250 AA; 26165 MW; E75A96708FCCFBB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                               PMRT: APY25922: AA189420.1; -.
Hypothetical protein.
SELUENTE - 44 AA; FOLLE MW; 854963B077EB881B ORO64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLIE). 16, Created)
51-MAR-2001 (TrEMBLIE). 15, Last Sequence update)
01-JUN-2002 (TREMBLIE). 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00761; SPASE_I_3; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGPFAMS; TIGROO162: Cons_hypoth62; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PET,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prcc. Natl. Acad. Sci. 5.S.A. 97.12
EMBL. Ac09500; AA019688.1; -
INTERPRO: IPP004426; Cons_hypoth62.
INTERPRO: IPR002766; UNF75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Halobacteriaceae, Halobacterium.
NCBI_TaxID=64091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ipponoso8: SigPTase.
                                                                                                                                                                                                                                                                                                                                                     Oncogene 20:5554-5561(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probom: PD008434; DUF75; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01908; DUF75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226 EEVVSRLQDMEE 237
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Best Local Similarity
7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EELMLRLQDYEE 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 HELMLRIQUYER 12
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                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome.
SEQUENCE 250 AR:
                                                                                                   NCBI_TaxID=31033;
                                                                                                                                                                                                                                                               Venkatesh B.;
                                                                                                                                                                                                                                                                                                                              evolutionary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vnq0546c.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OHBITO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9HRU0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9HRU0
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         % WERE BANK OF OF OF STANK AND STANK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal Month Light of the Month of the MEDIANE-917943; PubMed-10051754; Takahashi M., Yamanata M., Takahashi M., Yamanata M., Noda M.; "Specific expression of exrin, a cytoskeletal membrane linker protein, in a subset of chick relinstertal and sensory projections "; fur i Nourosci 11:545-558(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metaboa, Chordata, Craniata, Vertebrata, Euteleostomi)
Archosauria: Aves, Neognathae, Gallifornes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oy Supe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fügn rubripes (Japanese pufferfish) (Takifugu rubripvs).
Eukaryota: Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                            88.3%; Score 53; DB 11; Length 455; 83.3%; Pred, No. 0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75.0%; Score 45; DH 13; Length 5R5; 72.7%; Pred. No. 6.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE: PS00660; HAND_41_1, 1.
PROSITE: PS00661; RAND_41_2; 1.
PROSITE: PS00661; RAND_41_3; 1.
SEQUENCE: PS85 AA; BAND_41_3; 1.
SEQUENCE: PS85 AA; 69366 MW; M540634MP78407RP OPP44;
                                                                                                                                                                                                                                                                                                                       54174 MW. IFCGAGSF4C755893 CPC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  585 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           2, Mismatiches
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                                                                                                                                                                                   PROSITE; PSG6660; HAND_41_1; UNKNOWN_1.
PROSITE; PSG0661; HAND_41_2; UNKNOWN_1.
PROSITE; PSG0657; BAND_41_3; 1.
NON_TER 455 455
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01-DEC-2001 (FEMBLEEL 19, Last sequential and 2002 (FEMBLEEL 21, Last annot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-WHITE LEGHORN, TISSUE-BRAIN;
                                    Hz/rad/moesin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000299; Band_4.1.
InterPro; IPR000798; Ez/rad/moesin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical 60.2 kDa protein.
InterPro, IPPONO299, Mard_4 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB019790; BAA75497.1;
                                                                  Pfam, PF00373; Band_41; 1.
Pfam; PF00769; ERM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00373; Band_41; 1
Pfam; PF00769; ERM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00935; BAND41.
SMART; SM00295; B41; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                          PPINTS: PRO0935; BAND41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      345 EELMLRLQDFFQ 356
                                                                                                                                                           SMART; SM00295; B41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EELMLRLQDYEE 12
                                    IPE000738,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               345 RELLVRIQEYE 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EELMLRLQDYE 11
                                                                                                                                                                                                                                                                                                                 SEQUENCE 455 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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                                       interPro
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O9YCW6
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                                                                                                                                                                                                                                                                                                                                               Enkaryota; Metazea; Nematoda; Chromadorea; Rhabditida; Rhabditeidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical 48.1 Kbs protein (Fragment).
Homo sapiens (Human).
Enkaryota Metazoa: Chordata; Craniata: Vertebrata: Enteleostomi; Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
NOBL_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ċ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the nematode C. clegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 182:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ċ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3. Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: U29082; AAL02434.1; -.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             376 AA; 44436 MW; 93E32C5B13C4A6CE CEC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 429 AA: 48002 MW; D8D2471A95971E9A CRC64,
                                                                          01-DEC-2001 (FEMBLEEL 19, Created)
01-DEC-2001 (FEMBLEEL 19, Last sequence update)
01-JUN 2002 (FEMBLEEL 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P78514; 099844;
01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-1997 (TEMBLREL. 03, Last annotation update)
376 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  429 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The sequence of C. elegans cosmid C14F5.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      Rhabditidae; Peloderinae; Caenorhabditis.
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        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                          Hypothetical 44.4 kDa protein.
C14F5.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, U85995, AAB61919.1; -.
EMBL, U85994, AAB61918.1; -.
EMBL, U85997, AAB46606.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8: Conservative
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    PRELIMINARY;
                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 EEQHAKLQDYEE 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EELMIRLODYEE 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             œ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         None;
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2 ELMIRIQUYEE 12

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Kaneko T., Sato S., Kolani H., Tanaka A., Asamidu E., Nakamura Y., Miyajima N., Hirosawa M., Suqiura M., Susamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takcuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Segmence analysis of the genome of the unicellular eyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-96127529; pubMed-8590279; Arabko I., Mayajima N., Saroko I., Tanaka A., Sato S., Kotani H., Sazuka I., Mayajima N., Sugiura M., Tabata S.; Soquence analysis of the genome of the unicellular cyanobacterium "Soquence analysis of the genome of the unicellular cyanobacterium Synechocystis Sp. strain PCC6803. I. Sequence leatures in the 1 Mb region Irom map positions 64% to 92% of the genome."; DNA Res. 2:153-166(195).
                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryola; Melazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Romo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Positional candidates for the RP9 retinitis pigmentosa gene."; submitted (JAM-1997) to the EMBL/GenHank/DDHJ databases. EMBL: UB7408; AAN47568.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.0%; Score 39; DH 4; Length 453; 72.7%; Pred. No. 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 453 AA; 51050 MW; CSF53EE64A83D418 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria, Cyanobacteria, Chroococales, Synechocystis
                                                                                                                                                                                                                                        01-MAY-1997 (TYEMBLYEL, 03, Created)
01-MAY-1997 (TYEMBLYEL, 03, Last sequence update)
01-DEC-2001 (TYEMBLYEL, 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Bypothetical protein slr0031.
                                                                                                                                                                              453 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                             Hypothetical 51.1 kDa protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synechocystis sp. (strain PCC 6803).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 72.78
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
157 ELILRLQEYFE 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 ELMLRLQDYEE 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCB1_Tax1D-9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Keen I.J.
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                                                                                                     RESULT 11
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[1]
SEQUENCE FROM N.A.
TISSUE-OSTEOSARCOMA;
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                                                                                                                                                                                                                                                                                    Q9C6K2;
                                                                                                                                                                                                                                                                          09C6K2
                                                                                                                                                                                                                                                  RESULT 15
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                                                                                                                                                              Sign
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Submitted (MAY-1999) to the EMBL/GenBank/DDRJ databases
EMBL; AF155037; AAD43543.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIINE-99434236; PubMed-10502514; Mannisto R.H., Hamford J.K.; Mannisto R.H., Kivela H.M., Paulin L., Bamford D.H., Hamford J.K.; The complete genome sequence of PM2, the lirst lipid containing bacterial virus To Be isolated."; Virology 262:355-363(1999).
                                                                                                                                                                                                                                                                                                                                                           Viruses; dsDNA viruses, no RNA stage; Cortinoviridae; Corticovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryofa, Metazea, Cherdata, Graniata, Veitebiata, Euteleestomi,
Mammalia; Eutheria: Primates; Calarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ö
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C
                                                                                                                                                                                                                                                                                                                                                                                                         Kivela H M , Mannisto E H KallFinge N , Ramford D.H.; 
"purification and protein composition of PM2, the first lipid-
containing bacterial virus to be isolated."; 
Virology 0.0-0(1999)
                                                                                                                                   Score 39; DB 16; Length 584;
Pred No 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shore 39, DR 9, Langth 634,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; indels
                                                                                                                                                             1; Indels
                                                                     SMART: SM00228; PD2; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
Hypothetical protein; Complete proteome.
SEQUENCE: SH4 AA, NEWAR WW; PERSINGSE 4408 AF GRODEL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13543.1.) - .
72094 MW: - Brschloon4FEB2506 rpp:64 -
                                                                                                                                                                                                                                                                                             01-Nov-1999 (TrEMBLrel. 12, Created)
01-Nov-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Putative replication initiation protein P12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1999 (TrEMBLRel, 12, Created)
01-NOV-1999 (TrEMBLRel, 12, Last sequence update)
01-NOV-1999 (TrEMBLRel, 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  802 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIH-responsive osteosarcoma Bl protein.
                                                                                                                                                Pred No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                            MERGPS; mul.vol.
InterPro: IPRG01478; PHV.
InterPro: IPR00130; Zn_MTpeptdsc.
Plam: PF00545; PDZ; 1
ewapt: KM00228; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.68;
                                                                                                                                     65.0%;
                                                                                                                                                63.68
DNA Res. 3:109-136(1996).
EMBL; D64006; BAA10791.1:
                                                                                                                                   Query Match
Best Local Similarity 63.69
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 63.6
Matches 7: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                       PRFT.IMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
                                                                                                                                                                                                           521 EQLSLRLKDYQ 531
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                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10661;
                         MEROPS; M61.001;
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AEALINE=21016719; PubMed=11130712;

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AEALINE=21016719; PubMed=11130712;

AEALINE=21016719; PubMed=11130712;

AEALINE=2., Aleus A., Edeker J. R., Palulyo R., Bowman C.L., Brooks S.Y.,

AUGHLE D., Aleus J., Charay A.B., Cheny R.F., Chensy T.B.,

ADDING P., Edul P., Faldallyum T.V., Feng J.-D., Fong B., Fulli C.W.,

ADDING P., Edul P., Faldallyum T.V., Feng J.-D., Fong B., Fulli C.W.,

ADDING P., Edul P., Faldallyum T.V., Feng J.-D., Fong B., Fulli C.W.,

AND C.J., Acod H., J., Manasen D., Aleus B., Harizar L.,

AND Histopher J., Miranda M., Naryen M., Narviall A.,

AND Histopher J., Miranda M., Narviall A.,

AND Histopher J., Miranda M., Narviall A.,

Barano H., Salzerg S.L., Edul M., Edul M., Edul P., Coultwick A.M.,

San H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

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San H., Salzerg S.L., Schwartz J
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Fikaryota: Viridiplantae: Stroptophyta: Embrycphyta: Trachecphyta:
Spermatophyta: Madmollophyta, endicotyfedons, core endicots: Rosidae:
ectrosids II: Brassicales: Brassicaceae: Arabidopsis.
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MUDICINIC 99236731; PubMed-10221542; Adams A.B., Rosenblatt M., Suva L.J.; Adams A.B., Rosenblatt M., Suva L.J.; "Identification of a novel parathyroid hormone-respondive gene in human outerbolastic ells."; Bone 24:305-313(1969). EMBL: AR095771; AAD25981.1; -. SEQUENCE BOA AA; B9844 MW; 30785341940240A92 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                          Length 802;
                                                                                                                                                                                                                                                                                                                                55.0%; Score 39; DB 4; Length 802
72.7%; Pred. No. 1.1e+02;
wiemalches 1; Indels
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Hypothetical protein.
SEQUENCE 86 AA: 10022 MW: 0PF1E889823FB84B CHC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01 JUN 2001 (TrEMBLrel. 17, Created)
61-JUN-2061 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Job time : 44.7143 sees
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